



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/029,115	10/19/2001	Ying Luo	A-70229/RMS/DHR	2856

20350 7590 09/02/2004

TOWNSEND AND TOWNSEND AND CREW, LLP
TWO EMBARCADERO CENTER
EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

EXAMINER

GIBBS, TERRA C

ART UNIT	PAPER NUMBER
----------	--------------

1635

DATE MAILED: 09/02/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

10/029,115

Applicant(s)

LUO ET AL.

Examiner

Terra C. Gibbs

Art Unit

1635

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 14 June 2004.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 2,3 and 16-26 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 2,3 and 16-26 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>Sequence search alignments</u> . |

DETAILED ACTION

This Office Action is a response to Applicants Amendment and Remarks filed June 14, 2004.

Claims 1 and 4-15 have been canceled. Claims 2, 3, 16, and 17 have been amended. New claims 21-26 are acknowledged.

Claims 2, 3, and 16-26 have been examined on the merits.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Claim Rejections - 35 USC § 112

In the previous Office Action mailed March 9, 2004, claims 2 and 3 were rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. **This rejection is maintained** for the reasons of record set forth in the previous Office Action mailed March 9, 2004.

Response to Arguments

In response to this rejection, Applicants argue that claim 2 is now amended to recite a nucleic acid sequence having at least about 95% identity to SEQ ID NO:1, 3, or 5. Applicants argue that claim 2 has also been amended to recite that the nucleic acid, *and not its complement*, encodes a MINK3 protein.

This argument has been fully considered, but is not found persuasive because claims 2 and 3 still read on the *complement* of SEQ ID NO:1, 3, or 5 encoding a MINK3 protein. For

Art Unit: 1635

example, claims 2 and 3 are drawn to a recombinant nucleic acid, comprising a nucleic acid sequence having at least 95% identity to a nucleic acid sequences of SEQ ID NO:1, 3, and 5, **or complements thereof**, wherein said recombinant nucleic acid encodes a MINK3 protein. Therefore, the issue is would the *complement* of a recombinant nucleic acid comprising SEQ ID NOs:1, 3, and 5, encode a MINK3 protein as claimed? The Specification discloses SEQ ID NOs:1, 3, and 5 encode a MINK3 protein, but has not described a recombinant nucleic acid comprising SEQ ID NOs:1, 3, and 5, **or complements thereof**, which encode a MINK3 protein.

Applicant's amendment necessitated the new ground(s) of rejection presented below:

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

New claim 21 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. **This is a new written description rejection.**

Claim 21 is drawn to a recombinant nucleic acid, comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of

Art Unit: 1635

SEQ ID NOs: 1, 3, and 5, **or complements thereof**, wherein said recombinant nucleic acid encodes a MINK3 protein.

The issue is would the *complement* of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, encode a MINK3 protein as claimed? The instant Specification teaches SEQ ID NOs: 1, 3, and 5 encode a MINK3 protein. Applicants have not described a complement of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein.

Applicant is referred to the Guidelines on Written Description, published at FR 66(4) 1099-1111 (January 5, 2001) (also available at www.uspto.gov). The following passage is particularly relevant:

The written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species, by actual reduction to practice, reduction to drawings, or by disclosure of relevant identifying characteristics, i.e. structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between structure and function structure, or by a combination of such identifying characteristics, sufficient to show the Applicant was in possession of the claimed genus.

A "representative number of species" means that the species which are adequately described are representative of the entire genus. Thus, when there is substantial variation within a genus, one must describe a sufficient number of species to reflect the variation within the genus. What constitutes a "representative number" is an inverse function of the skill and knowledge in the art. Satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that Applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed. In an unpredictable art, adequate written description of a genus which embraces widely variant species cannot be achieved by disclosing only one species within the genus.

The central issue of this rejection is whether Applicant has described a sufficient number of species to adequately represent the genus of complement recombinant nucleic acids comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence

Art Unit: 1635

selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein. It is unclear how the *complement* of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, will encode a MINK3 protein as claimed. It is recognized in the prior art that the function of a protein depends on the sequence of its amino acids in a certain pattern, conformation of the protein due to the amino acid sequence, and the functional properties of the different parts of the protein (see second paragraph in Rudinger J in Peptide Hormones. Editor Parsons JA. Pages 1-7, 1976, University Park Press, Baltimore). Rudinger further add, "The significance of particular amino acids and sequences for different aspects of biological activity can not be predicted *a priori* but must be determined from case to case by painstaking experimental study" (see conclusion on page 6).

In summary, the Specification teaches SEQ ID NOs:1, 3, and 5 encode a MINK3 protein, but has not described the complement of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein. In view of the number of disclosed species, and the failure to provide the structure and physical properties of the complement of a recombinant nucleic acid comprising a nucleic acid sequence having at least 98% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1, 3, and 5, which encodes a MINK3 protein, which would allow one to accurately predict the recombinant nucleic acids which possess such activity, one of skill in the art would conclude that Applicant was not in possession of the claimed invention at the time of filing.

Claim Rejections - 35 USC § 102

In the previous Office Action mailed March 9, 2004, claims 2, 3, and 16-18 were rejected under 35 U.S.C. 102(b) as being anticipated by Ippeita et al. (FEBS Letters, 2000 Vol. 469:19-23). **This rejection is maintained** for the reasons of record set forth in the previous Office Action.

Response to Arguments

In response to this rejection, Applicants argument is three-fold. First, Applicants argue that to anticipate a claim, the reference must teach every element of the claims. Second, Applicants argue that claim 2 has been amended to recite a nucleic acid having greater than about 95% identity to SEQ ID NO:1, 3, or 5, and this amendment obviates the instant rejection. Third, Applicants argue that claim 16 is directed to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. Applicants argue that the Office Action appears to incorrectly assert that the MINK3 polypeptide of SEQ ID NO:2 of the instant invention contains the full amino acid sequence of the MINK1 protein of Ippeita et al. in combination with additional amino sequences. Applicants contend that nucleobases 1738-1798 of MINK1 are not present in SEQ ID NO:1, and because SEQ ID NO:2 does not include all the sequences of the cited MINK1, claim 16 and dependent claims 17-20 are not anticipated by Ippeita et al.

Art Unit: 1635

This argument has been fully considered, but is not found persuasive. First regarding Applicants first argument, the cited art teaches every element of the instant claims. For example, [and in response to Applicants second argument] claim 2 has been amended to recite a recombinant nucleic acid, comprising a nucleic acid sequence having at least 95% identity to a nucleic acid sequences of SEQ ID NO:1, 3, and 5, or complements thereof, wherein said recombinant nucleic acid encodes a MINK3 protein. Ippeita et al. disclose the molecular cloning of MINK1 (see Figure 2). The nucleotide sequence of MINK1 is over 96% identical to SEQ ID NO:1 of the instant invention (see attached sequence alignment), and thus meets the limitations of claim 2 and dependent claim 3. Regarding Applicants third argument, claim 16 is drawn to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. The MINK1 disclosure of Ippeita et al. further meets the limitations of claim 16 because the amino acid sequence of MINK1 is almost 99% identical to SEQ ID NO:2 of the instant invention (see attached sequence alignment), and thus meets the limitations of claim 16 and dependent claims 17 and 18.

Therefore, Ippeita et al. anticipate claims 2, 3, and 16-18.

In the previous Office Action mailed March 9, 2004, claims 2, 3, and 16-18 were rejected under 35 U.S.C. 102(b) as being anticipated by Plowman et al. [U.S. Patent No. 6,656,716] ('716 Patent). **This rejection is maintained** for the reasons of record set forth in the previous Office Action.

Response to Arguments

In response to this rejection, Applicants argument is three-fold. First, Applicants argue that to anticipate a claim, the reference must teach every element of the claims. Second, Applicants argue that claim 2 has been amended to recite a nucleic acid having greater than about 95% identity to SEQ ID NO:1, 3, or 5, and this amendment obviates the instant rejection. Third, Applicants argue that claim 16 is directed to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. Applicants argue that the Office Action appears to incorrectly assert that the MINK3 polypeptide of SEQ ID NO:2 of the instant invention contains the full amino acid sequence of the ZC3 protein of Plowman et al. in combination with additional amino sequences. Applicants contend that residues 582-602 are not present in SEQ ID NO:2 and because SEQ ID NO:2 does not include all the sequences of the cited ZC3, claim 16 and dependent claims 17-20 are not anticipated by Plowman et al.

This argument has been fully considered, but is not found persuasive. First regarding Applicants first argument, the cited art teaches every element of the instant claims. For example, [and in response to Applicants second argument] claim 2 has been amended to recite a recombinant nucleic acid, comprising a nucleic acid sequence having at least 95% identity to a nucleic acid sequences of SEQ ID NO:1, 3, and 5, or complements thereof, wherein said recombinant nucleic acid encodes a MINK3 protein. The '716 Patent discloses the nucleotide sequence of human ZC3 (see SEQ ID NO:11 and Figure 9J), which is over 95% identical to SEQ ID NO:1 of the instant invention (see attached sequence alignment), and thus meets the

Art Unit: 1635

limitations of claim 2 and dependent claim 3. Regarding Applicants third argument, claim 16 is drawn to nucleic acids that encode a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of the amino acid sequences set forth in SEQ ID NOs: 2, 4, and 6. The ZC3 disclosure of Plowman et al. further meets the limitations of claim 16 because the amino acid sequence of ZC3 is almost 96% identical to SEQ ID NO:2 of the instant invention (see attached sequence alignment), and thus meets the limitations of claim 16 and dependent claims 17 and 18.

Therefore, Plowman et al. anticipate claims 2, 3, and 16-18.

Applicant's amendment necessitated the new ground(s) of rejection presented below:

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claim 19, 20, and new claims 22-26 are rejected under 35 U.S.C. 102(b) as being anticipated by Ippeita et al. (FEBS Letters, 2000 Vol. 469:19-23). **This is a new rejection.**

Claim 19 is drawn to a method of making a MINK3 protein comprising culturing a host cell comprising a recombinant nucleic acid, comprising a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of SEQ ID NOs: 2, 4, and 6, under conditions suitable for

Art Unit: 1635

the expression of MINK3. Claim 20 is dependent on claim 19 and includes all the limitations of claim 19, with the further step of isolating the MINK3 protein. Claim 22 is drawn to a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence having at least 98% identity to an amino acid selected from the group consisting of SEQ ID NOs: 2, 4, and 6. Claim 23 is drawn to a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, and 6. Claims 24-26 are drawn to a nucleic acid sequence that encodes a MINK3 protein comprising an amino acid sequence having at least 95% identity to an amino acid selected from the group consisting of SEQ ID NOs: 2, 4, and 6, wherein the MINK3 protein activates a(n) JNK and ERK, and binds to a Nck protein.

Ippeita et al. disclose the molecular cloning of MINK1 (see Figure 2). The nucleotide sequence of MINK1 is over 96% identical to SEQ ID NO:1 of the instant invention (see attached sequence alignment), while the amino acid sequence of MINK1 is over 99% identical to SEQ ID NO:2 of the instant invention (see attached sequence alignment), and thus meets the limitations of claims 22 and 23. Ippeita et al. disclose full length MINK1 was cloned into a pCMV expression vector and transiently expressed in HEK 293 cells (see Figure 5A) and thus meets the limitations of claims 19 and 20. Ippeita et al. further disclose the kinase activity of MINK1, and show that MINK1 activates JNK and ERK proteins (see Figures 5B and 5D, respectively). It is noted that Ippeita et al. do not disclose that MINK1 binds to a Nck protein. However, at page 20, second column, Ippeita et al. disclose that it is likely that MINK1 interacts with Nck because the two share conserved binding regions. Therefore, absent evidence to the contrary, MINK1 binds to a Nck protein.

Art Unit: 1635

Therefore, claims 19, 20, and 22-26 are anticipated by Ippeita et al.

Conclusion

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire **THREE MONTHS** from the mailing date of this action. In the event a first reply is filed within **TWO MONTHS** of the mailing date of this final action and the advisory action is not mailed until after the end of the **THREE-MONTH** shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than **SIX MONTHS** from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Terra C. Gibbs whose telephone number is (571) 272-0758. The examiner can normally be reached on M-F 9:00-5:00.

Art Unit: 1635

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John L. LeGuyader can be reached on (571) 272-0760. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

tcg

September 1, 2004



JOHN L. LeGUYADER
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Sequence search alignment. ..

Applicants Copy

ALIGNMENTS

RESULT 1

M4K6_HUMAN

ID M4K6_HUMAN STANDARD; PRT; 1332 AA.

AC Q8N4C8; Q9P1X1; Q9P2R8;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Mitogen-activated protein kinase kinase kinase kinase 6 (EC 2.7.1.37)

DE (MAPK/ERK kinase kinase kinase 6) (MEK kinase kinase 6) (MEKKK 6)

DE (Misshapen/NIK-related kinase) (GCK family kinase MINK).

GN MAP4K6 OR MINK.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

RC TISSUE=Brain;

RX MEDLINE=20175403; PubMed=10708748;

RA Dan I., Watanabe N.M., Kobayashi T., Yamashita-Suzuki K., Fukagaya Y.,

RA Kajikawa E., Kimura W.K., Nakashima T.M.; Matsumoto K.,

RA Ninomiya-Tsuji J., Kusumi A.;

RT "Molecular cloning of MINK, a novel member of mammalian GCK family

RT kinases, which is up-regulated during postnatal mouse cerebral

RT development.";

RL FEBS Lett. 469:19-23 (2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 3).

RC TISSUE=Lymph;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -!- FUNCTION: Serine/threonine kinase that may play a role in the

CC response to environmental stress. Appears to act upstream of the

CC c-jun N-terminal pathway (By similarity).

CC -!- FUNCTION: May play a role in the development of the brain (By

CC similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a prptein = ADP + a

Sequence search alignment...

Applicants Copy

ALIGNMENTS

RESULT 1

US-09-688-188B-15
; Sequence 15, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-688-188B-15

Query Match 96.1%; Score 6659; DB 4; Length 1326;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1270; Conservative 3; Mismatches 3; Indels 50; Gaps 3;

```
QY      36 YGQVYKGRHVKTGQLAAIKVMDVTEDEEEIKQEIINMLKKYSHHRNIATYYGAFIKKSPP 95
       123456789012345678901234567890123456789012345678901234567890
Db      2 FGEVYEGRHVKTGQLAAIKVMDVTEDEEEIKQEIINMLKKYSHHRNIATYYGAFIKKSPP 61

QY      96 GNDDQLWLVMEFCGAGSVTDLVKNTKGNALKEDCIAIYICREILRGLAHLHAHKVIHRDIK 155
       123456789012345678901234567890123456789012345678901234567890
Db      62 GNDDQLWLVMEFCGAGSVTDLVKNTKGNALKEDCIAIYICREILRGLAHLHAHKVIHRDIK 121

QY     156 GQNVLLTENAEBVKLVDFGVSAQLDRTVGRRNTFIGTPYWMapeviACDENPDATYDYRSD 215
       123456789012345678901234567890123456789012345678901234567890
Db     122 GQNVLLTENAEBVKLVDFGVSAQLDRTVGRRNTFIGTPYWMapeviACDENPDATYDYRSD 181

QY     216 IWSLGITAIEAEGAPPLCDMHPMRALFLIPRNPPLKSKKWSKKFIDFIDTCLIKTYL 275
       123456789012345678901234567890123456789012345678901234567890
Db     182 IWSLGITAIEAEGAPPLCDMHPMRALFLIPRNPPLKSKKWSKKFIDFIDTCLIKTYL 241

QY     276 SRPPTQLLKFPFIRDOPTERQVRIQLKDHIDRSRKKRGEKEETEYEGSGSEEDDSHGE 335
       123456789012345678901234567890123456789012345678901234567890
Db     242 SRPPTQLLKFPFIRDOPTERQVRIQLKDHIDRSRKKRGEKEETEYEGSGSEEDDSHGE 301

QY     336 EGEPSSIMNVPGESTLRRFLRLQQENKSNSEALKQQQQQLQQQQORDPEAHIKHLLHQRQ 395
       123456789012345678901234567890123456789012345678901234567890
```

Mon Aug 30 09:54:25 2004

us-10-029-1

Db 302 EGEPSIMNVPGESTLRRREFLRLQQENKSNSEALKQOOOLQOOQQRDPEAHIKHLLHQRQ 361
Qy 396 RRIEEQKEERRRVEEQORREREQRKLOEKEQORRLEDQALRREEERRQAEREQ----- 449
|||
Db 362 RRIEEQKEERRRVEEQORREREQRKLOEKEQORRLEDQALRREEERRQAEREQEIYIRHR 421
Qy 450 -----EYKRKQLEEQRQSERLQRLQOEHAYLKSLLQOOQQQ 486
|||
Db 422 LEEEQRLLEILQOQLQOEQALLLEYKRKQLEEQRQSERLQRLQOEHAYLKSLLQOOQQQ 481
Qy 487 QLQKQQQQQLLPGRKPLYHYGRGMNPADKPAWAREVEERTRMNKQONSPLAKSKPGSTG 546
|||
Db 482 QLQKQQQQQLLPGRKPLYHYGRGMNPADKPAWAREVEERTRMNKQONSPLAKSKPGSTG 541
Qy 547 PEPPIPQASPGPPGPLSQTTPMQRVPEPQEGPHK-----SLQDQP 586
|||
Db 542 PEPPIPQASPGPPGPLSQTTPMQRVPEPQEGPHKSLVAHRVPLKPYAAPVPRSQSLQDQP 601
Qy 587 TRNLAAFPASHDPDAIPAPTATPSARGAVIRQNSDPTSEGGPSPNPPAWVRPDNEAPP 646
|||
Db 602 TRNLAAFPASHDPDAIPAPTATPSARGAVIRQNSDPTSEGGPSPNPPAWVRPDNEAPP 661
Qy 647 KVPQRTSSIATALNTSGAGGSRPAQAVRARPRNSAWQIYLQRRARERTPKPPGPPAQPP 706
|||
Db 662 KVPQRTSSIATALNTSGAGGSRPAQAVRARPRNSAWQIYLQRRARERTPKPPGPPAQPP 721
Qy 707 GPPNASSNPDLRRSDPGWERSDSVLPASHGHLPOAGSLERNRVGASSKLDSSPVLSPGNK 766
|||
Db 722 GPPNASSNPDLRRSDPGWERSDSVLPASHGHLPOAGSLERNRVGVSSKPDSSPVLSPGNK 781
Qy 767 AKPDDHRSRPGRPADFVLLKERTLDEAPRPPKKAMDYSSSSEEVESSEDDEEEGEGGP 826
|||
Db 782 AKPDDHRSRPGRPADFVLLKERTLDEAPRPPKKAMDYSSSSEEVESSEDDEEEGEGGP 841
Qy 827 GSRDTPGGRSDGDTDSVSTMVVDVEEITGTQPPYGGGTMVVQRTPEEERNLLHADSNGY 886
|||
Db 842 GSRDTPGGR-DGDTDSVSTMVVDVEEITGTQPPYGGGTMVVQRTPEEERNLLHADSNGY 900
Qy 887 TNLPDVVQPSHSPTENSKGQSPPSKDGSGDYQSRGLVKAPGKSSFTMFVDLGIYQPGSG 946
|||
Db 901 TNLPDVVQPSHSPTENSKGQSPPSKDGSGDYQSRGLVKAPGKSSFTMFVDLGIYQPGSG 960
Qy 947 DSIPITALVGGEGTRLDQLQYDVRKGSVVNNPTNTRAHSETPEIRKYKKRFNSEILCAA 1006
|||
Db 961 DSIPITALVGGEGTRLDQLQYDVRKGSVVNNPTNTRAHSETPEIRKYKKRFNSEILCAA 1020
Qy 1007 LWGVNLLVGTENGLMLLDRSGQGVYGLIGRRRFQOMDVLEGLNLLITISGKRNLKVY 1066
|||
Db 1021 LWGVNLLVGTENGLMLLDRSGQGVYGLIGRRRFQOMDVLEGLNLLITISGKRNLKVY 1080
Qy 1067 LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK 1126
|||
Db 1081 LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK 1140
Qy 1127 PYHKFMAFKSFADLPHRPLLVDLTVEEQRLKVIYGSSAGFHAVDVDSGNSYDIYIPVHI 1186
|||
Db 1141 PYHKFMAFKSFADLPHRPLLVDLTVEEQRLKVIYGSSAGFHAVDVDSGNSYDIYIPVHI 1200
Qy 1187 OSQITPHAIIFLNTDGMEMLLCYEDEGVVNTYGRIIKDVVLQWGEMPTSVAYICSNQI 1246
|||
Db 1201 OSQITPHAIIFLNTDGMEMLLCYEDEGVVNTYGRIIKDVVLQWGEMPTSVAYICSNQI 1260
Qy 1247 MGWGEKAIEIRSVETGHLGDFVFMHKRAQLKFLCERNKVFFASVRSGGSSQVYFMTLNR 1306
|||
Db 1261 MGWGEKAIEIRSVETGHLGDFVFMHKRAQLKFLCERNKVFFASVRSGGSSQVYFMTLNR 1320
Qy 1307 NCIMNW 1312
|||
Db 1321 NRIMNW 1326

Applicants Copy

AUTHORS Dan, I., Watanabe, N.M. and Kusumi, A.

Query Match	96.3%	Score 3803.2	DB 1	Length 3888
Best Local Similarity	95.6%	Prod. No. 0		
Matches 3825	Conservative	0	Mismatches 3	Indels 171
Gaps	2			
QY	7	ATGGGACCCAGCCCGCCCGCGAGCTGGACGACATCGACCTGTGCGCCCTCGGGGAC	66	
DB	1	ATGGGACCCAGCCCGCCCGCGAGCTGGACGACATCGACCTGTGCGCCCTCGGGGAC	60	
QY	67	CTTGCTGGGATCTTTGAGCTTGTGGAGGTGGTTCGGCAATGGAACTACGGACAGGTGAC	126	
DB	61	CTTGCTGGGATCTTTGAGCTTGTGGAGGTGGTTCGGCAATGGAACTACGGACAGGTGAC	120	
QY	127	AAGGTCGGCATGTCAAGACGGGGCAGCTGGTCGCATCAAGGTCAATGATCACGGAG	186	
DB	121	AAGGTCGGCATGTCAAGACGGGGCAGCTGGTCGCATCAAGGTCAATGATGTCAAGGAG	180	
QY	187	GACGAGGAGGACGAGATCAAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACACCGC	246	
DB	181	GACGAGGAGGAGGATCAAAACAGGAGATCAACATGCTGAAAAAGTACTCTCACACCGC	240	
QY	247	AACATCGCCACTACTACGGAGCCTTCATCAAGAAAGCCCCCGGAAACGATGACCCAG	306	

Db 241 AACATGCCACCTACTACGAGGCTTCAATCAAGAGAGGCCCCCGGAAAAACGATGCCAG 300
Qy 307 CTCTGGCTGTGATGAGTTCTCTGTGTGTGTTCACTGACTGACCTGTGTAAAGAACACA 366
Db 301 CTCTGGCTGTGATGAGTTCTGTGTGTGTGTTCACTGACTGACCTGTGTAAAGAACACA 360
Qy 367 AAAGGCAACCCCTGTAAGGAGGACTGTATGCGCTATATCTTGCAGGGAGATCTCTCAGGGGT 426
Db 361 AAAGGCAACCCCTGTAAGGAGGACTGTATGCGCTATATCTTGCAGGGAGATCTCTCAGGGGT 420
Qy 427 CTGSCCATCTCCATGCCCAAGAGTGCATCCATCGAGACATCAAGGGGAGATGTGTG 486
Db 421 CTGSCCATCTCCATGCCCAAGAGTGCATCCATCGAGACATCAAGGGGAGATGTGTG 480
Qy 487 CTGACAGAGAACTCTGAGGTCAAGTCTAGTGGATTTTGGGTGAGTCTCTAGGA 546
Db 481 CTGACAGAGAACTCTGAGGTCAAGTCTAGTGGATTTTGGGTGAGTCTCTAGGA 540
Qy 547 ACCGTGGCAGCGGACACTTTCAATGGGACTCCCTACTGATGGCTCCAGAGTCAATC 606
Db 541 ACCGTGGCAGCGGACACTTTCAATGGGACTCCCTACTGATGGCTCCAGAGTCAATC 600
Qy 607 GCCTGTGATGAGAACCTGTATGCCACCTATGATTACAGGAGTGATTTTGGTCTCTAGGA 666
Db 601 GCCTGTGATGAGAACCTGTATGCCACCTATGATTACAGGAGTGATTTTGGTCTCTAGGA 660
Qy 667 ATCACAGCATCGAGATGGCAGAGGAGGCCCCCTCTGTGTGACATGACCCCATGCGA 726
Db 661 ATCACAGCATCGAGATGGCAGAGGAGGCCCCCTCTGTGTGACATGACCCCATGCGA 720
Qy 727 GCCTCTTCTCTATCTCGGAACCTCTCGGCCAGGCTCAAGTCCAAAGAGTGTCTAAG 786
Db 721 GCCTCTTCTCTATCTCGGAACCTCTCGGCCAGGCTCAAGTCCAAAGAGTGTCTAAG 780
Qy 787 AAGTTCAATGACTTCATGACATGCTCTCATCAAGACTTACTGAGCCGCCACCCAG 846
Db 781 AAGTTCAATGACTTCATGACATGCTCTCATCAAGACTTACTGAGCCGCCACCCAG 840
Qy 847 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCCAGCCAGCGAGGCGGAGTCCGCATC 906
Db 841 GAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCCAGCCAGCGAGGCGGAGTCCGCATC 900
Qy 907 CAGTTAAGACACATTTGACCGGATCCCGGAAAGAGCGGGGTGAGAAAGAGAGACAGAA 966
Db 901 CAGTTAAGACACATTTGACCGGATCCCGGAAAGAGCGGGGTGAGAAAGAGAGACAGAA 960
Qy 967 TATGAGTACAGCGGACGAGGAGGAGATGACAGCCATGGAGAGAGAGAGAGCCAGC 1026
Db 961 TATGAGTACAGCGGACGAGGAGGAGATGACAGCCATGGAGAGAGAGAGAGCCAGC 1020
Qy 1027 TCCATCATGAACCTGCTGGAGAGTGCATCTACGCCGGGAGTTTCTCCGGGTCCAGCAG 1086
Db 1021 TCCATCATGAACCTGCTGGAGAGTGCATCTACGCCGGGAGTTTCTCCGGGTCCAGCAG 1080
Qy 1087 GAAATTAAGACAACTCAGAGGCTTTAAACAGCAGCAGCAGAGTGCAGCAGCAGCAG 1146
Db 1081 GAAATTAAGACAACTCAGAGGCTTTAAACAGCAGCAGCAGCAGTGCAGCAGCAGCAG 1140
Qy 1147 CGAGACCCCGAGGACACATCAACACCTGCTGCACAGCGGCGAGCGGCATAGAGGAG 1206
Db 1141 CGAGACCCCGAGGACACATCAACACCTGCTGCACAGCGGCGAGCGGCATAGAGGAG 1200
Qy 1207 CAGAGGAGAGCGGCGCGCTGGAGAGAGCAACAGCGGCGGAGCGGAGCAGCGGAAG 1266
Db 1201 CAGAGGAGAGCGGCGCGCTGGAGAGAGCAACAGCGGCGGAGCGGAGCAGCGGAAG 1260
Qy 1267 CTGACGAGAGAGCAGCAGCGCGCTGGAGAGCATGCGGCTCTCGCGCGGAGGAG 1326
Db 1261 CTGACGAGAGAGCAGCAGCGCGCTGGAGAGCATGCGGCTCTCGCGCGGAGGAG 1320
Qy 1327 GAGCGGCGGAGCGGAGCGTGTAGCGAGGAATAAAGCGGAGCAGCTGGAGGAGCGG 1386
Db 1321 GAGCGGCGGAGCGGAGCGGAGCGAGGAATAAAGCGGAGCAGCTGGAGGAGCGG 1380

Qy 1387 CAGTCAGAACTCTCCAGAGGCGAGCTGCACAGAGCATGCCTACCTCAAGTCCCTGCAG 1446
Db 1381 CAGTCAGAACTCTCCAGAGGCGAGCTGCAGAGGAGCATGCCTACCTCAAGTCCCTGCAG 1440
Qy 1447 CAGCAGCAACAGCAGCAGCAGCTTTCAGAAACAGCAGCAGCAGCAGCTCTCTGCTGGGGAC 1506
Db 1441 CAGCAGCAACAGCAGCAGCAGCAGCTTTCAGAAACAGCAGCAGCAGCAGCTCTCTGCTGGGGAC 1500
Qy 1507 AGNAGGCCCTGTACCAATATGTGTGGGGCATGAATCCCGCTGACAAACAGGCTGGGCC 1566
Db 1501 AGAAGGCCCTGTACCAATATGTGTGGGGCATGAATCCCGCTGACAAACAGGCTGGGCC 1560
Qy 1567 CGAGAGTAGAAGAGAGAAACAAGGATGAACAAGCAGCAGAACTCTCTCTTGGCCAAGAG 1626
Db 1561 CGAGAGTAGAAGAGAGAAACAAGGATGAACAAGCAGCAGAACTCTCTCTTGGCCAAGAG 1620
Qy 1627 AAGCCAGCAGCAGCGGGCTTGAAGCCCTTATCCCTAGGCTTCCCGAGGCTCCCGAG 1686
Db 1621 AAGCCAGCAGCAGCGGGCTTGAAGCCCTTATCCCTAGGCTTCCCGAGGCTCCCGAG 1680
Qy 1687 CCCCCTTCCAGACTCTCTCTATGACAGAGCCCGGTGGAGCCCGCAGAGGAGCCGCAACA 1744
Db 1681 CCCCCTTCCAGACTCTCTCTATGACAGAGCCCGGTGGAGCCCGCAGAGGAGCCGCAACA 1740
Qy 1745 -----AG 1746
Db 1741 AGCCTGTGSCACACCGGCTCCCACTGAAGCCATATGACAGCACTGTATCCCGATCCAG 1800
Qy 1747 TCCCTGACGAGCAGCGCCACCCGAAACCTTGGCTGTCTTCCAGCTTCCCATGACCCCGAC 1806
Db 1801 TCCCTGACGAGCAGCGCCACCCGAAACCTTGGCTGTCTTCCAGCTTCCCATGACCCCGAC 1860
Qy 1807 CTGCGCATCCCGGACCCCATGCGCAGCGGCTGCGAGGAGCTGTATCCGCGCAAGAT 1866
Db 1861 CCTGCCATCCCGGACCCCATGCGCAGCGGCTGCGAGGAGCTGTATCCGCGCAAGAT 1920
Qy 1867 TCAGACCCCACTCTGAAGGACCTGCGCCAGCCGCAATCCCGCAGCTGGGTCCGCCCA 1926
Db 1921 TCAGACCCCACTCTGAAGGACCTGCGCCAGCCGCAATCCCGCAGCTGGGTCCGCCCA 1980
Qy 1927 GATTAACGAGCCCAACCCAAAGTGTCTTCAGAGGACCTCTATCTATCGCCACTGTCCCTTAAC 1986
Db 1981 GATTAACGAGCCCAACCCAAAGTGTCTTCAGAGGACCTCTATCTATCGCCACTGTCCCTTAAC 2040
Qy 1987 ACCAGTGGGCGGAGGCTCCCGGCGCAGCCAGCGAGTCCGTGCCAGACCTCGCAGCAAC 2046
Db 2041 ACCAGTGGGCGGAGGCTCCCGGCGCAGCCAGCGAGTCCGTGCCAGCTCCGTGCC 2085
Qy 2047 TCCGCTTGGCAAACTCTATCTGCAAAAGGCGGCGAGAGCGGCGCACCCCAAGCCTCCAGGG 2106
Db 2086 ----- 2085
Qy 2107 CCCCCTGCTCAGCCCCCTGSCCGCCGCAAGCGCTCTAGTAAACCCCGACCTCAGGAGGAGC 2166
Db 2086 -----AGTAAACCCCGACCTCAGGAGGAGC 2109
Qy 2167 GACCCCTGGTGGAACCGCTCGGACAGCGTCTTTCAGCGCTCTCAGCGGACACCTCCCGCAG 2226
Db 2110 GACCCCTGGTGGAACCGCTCGGACAGCGTCTTTCAGCGCTCTCAGCGGACACCTCCCGCAG 2169
Qy 2227 GCTGGGCTCACTGGAGCGGAACCGCGTGGGAGCTCTCTCCAAACTGACAGCTCCCTGTG 2286
Db 2170 GCTGGGCTCACTGGAGCGGAACCGCGTGGGAGTCTCTCTCCAAACCGGACAGCTCCCTGTG 2229
Qy 2287 CTCTCCCTCGGGAATAAGGCAAGCCCGCAGACACCGCTCAGCGGCGAGCGCGGCCGCA 2346
Db 2230 CTCTCCCTCGGGAATAAGGCAAGCCCGCAGACACCGCTCAGCGGCGAGCGCGGCCGCA 2289
Qy 2347 GACTTTGTGTGTGAAGAGCGGAGCTGTGGAAGAGGCCCTCTGGCTCCCAAGAGAGGCC 2406
Db 2290 GACTTTGTGTGTGAAGAGCGGAGCTGTGGAAGAGGCCCTCTGGCTCCCAAGAGAGGCC 2349

```
QY 2407 ATGGACTACTCTGCTCCAGCGAGAGGTGGAAAGCAGCTAGGAGCAGCGAGGAGGAAGGC 2466
Db 2350 ATGGACTACTCTGCTCCAGCGAGAGGTGGAAAGCAGCTAGGAGCAGCGAGGAGGAAGGC 2409
QY 2467 GAAAGCGGCGCAGCAGAGGGAGCAGAGATACCCCTGGGGGCGCAGCGATGGGGATACA 2526
Db 2410 GAAAGCGGCGCAGCAGAGGGAGCAGAGATACCCCTGGGGGCGCAGCGATGGGGATACA 2469
QY 2527 GACAGGTCAGCACCAATGCTGTGTCACAGAGTCGAGAGGATACAAGGAGCCAGCCGCCA 2586
Db 2470 GACAGGTCAGCACCAATGCTGTGTCACAGAGTCGAGAGGATACAAGGAGCCAGCCGCCA 2529
QY 2587 TACGGGGGGCGCAGCAGATGCTGTGTCAGCGCACCCCTGAAAGAGGAGCGGAACTGTGTCAT 2646
Db 2530 TACGGGGGGCGCAGCAGATGCTGTGTCAGCGCACCCCTGAAAGAGGAGCGGAACTGTGTCAT 2589
QY 2647 GTGTACAGCAATGGGTGACACAAACCTGCTGTGTCAGGTGTCAGCCAGCCATCACCCACC 2706
Db 2590 GCTGTACAGCAATGGGTGACACAAACCTGCTGTGTCAGGTGTCAGCCAGCCATCACCCACC 2649
QY 2707 GAGAACAGCAAGAGCCCAAGGCCACCCCTCGAAGGATGGAGTGGTGACTACCAAGTCTCGT 2766
Db 2650 GAGAACAGCAAGAGCCCAAGGCCACCCCTCGAAGGATGGAGTGGTGACTACCAAGTCTCGT 2709
QY 2767 GGGCTGGTAAAGGCCCTTGGCAAGAGCTCGTTTACGATGTTTGTGGATCTAGGGATCTAC 2826
Db 2710 GGGCTGGTAAAGGCCCTTGGCAAGAGCTCGTTTACGATGTTTGTGGATCTAGGGATCTAC 2769
QY 2827 GAGCCTGGAGGCGAGTGGGAGCAGCATCCCATCACAGCCCTAGTGGTGGAGAGGGCACT 2886
Db 2770 GAGCCTGGAGGCGAGTGGGAGCAGCATCCCATCACAGCCCTAGTGGTGGAGAGGGCACT 2839
QY 2887 CGGCTCGACAGCTGTCAGTACGACGTGAGGAGAGGTTCGTGGTCAAGCTGAATCCCAACC 2946
Db 2830 CGGCTCGACAGCTGTCAGTACGAGGTGAGGAGAGGTTCGTGGTCAAGCTGAATCCCAACC 2889
QY 2947 AACACCCGGGCGCAGTAGTGAGACCCCTGAGATCGGAGTAGTCAAGAGCGGATTCAACTCC 3006
Db 2890 AACACCCGGGCGCAGTAGTGAGACCCCTGAGATCGGAGTAGTCAAGAGCGGATTCAACTCC 2949
QY 3007 GAGATCCTCTGTGACGCCCTTTGGGGGTCAACTGCTGGTGGGACGAGAAAGGGGTG 3066
Db 2950 GAGATCCTCTGTGACGCCCTTTGGGGGTCAACTGCTGGTGGGACGAGAAAGGGGTG 3009
QY 3067 ATGTTGCTGGACGAGAGTGGGACGAGGCAAGGTGTATGGAATCATTTGGGGCGGCAAGCTTC 3126
Db 3010 ATGTTGCTGGACGAGAGTGGGACGAGGCAAGGTGTATGGAATCATTTGGGGCGGCAAGCTTC 3069
QY 3127 GAGCAGATGGATGTGCTGGAGGGGCTCAACTGCTCATCAACCATCTCAGGGAAAGGAAC 3186
Db 3070 GAGCAGATGGATGTGCTGGAGGGGCTCAACTGCTCATCAACCATCTCAGGGAAAGGAAC 3129
QY 3187 AAACTGGGGTGTATTACCTGCTCTGGCTCGGAAACAAGATTCTGCACAATGACCCAGAA 3246
Db 3130 AAACTGGGGTGTATTACCTGCTCTGGCTCGGAAACAAGATTCTGCACAATGACCCAGAA 3189
QY 3247 GTGGAGAAAGCAGGGCTGGACCAACGTTGGGGACATGGAGGGCTCGGGGCACTACCGT 3306
Db 3190 GTGGAGAAAGCAGGGCTGGACCAACGTTGGGGACATGGAGGGCTCGGGGCACTACCGT 3249
QY 3307 GTTGTGAATACAGCGGATTAAGTTTCCTGCTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3366
Db 3250 GTTGTGAATACAGCGGATTAAGTTTCCTGCTCATCGCCCTCAAGAGCTCCGTGGAGGTG 3309
QY 3367 TATGCTGGGCCCCCAAAACCTTACCAAAATTCATGGCCCTTCAAGTCCCTTTCGGCACTTC 3426
Db 3310 TATGCTGGGCCCCCAAAACCTTACCAAAATTCATGGCCCTTCAAGTCCCTTTCGGCACTTC 3369
QY 3427 CCCCAACCGCCCTCTGCTGCTGCACTTACAGTACAGAGGGGCGAGCGGCTCAAGTTCATC 3486
Db 3370 CCCCAACCGCCCTCTGCTGCTGCACTTACAGTACAGAGGGGCGAGCGGCTCAAGTTCATC 3429
QY 3487 TATGGCTCCAGTGTGGCTTCCATGTGCTGTGATGTGCACTCGGGGAAACGCTATGACATC 3546
```

```
Db 3430 TATGGCTCCAGTGTCTGGCTTCCATGCTGTGGATGTGACTCGGGGAACAGCTATGACATC 3489
QY 3547 TACATCCCTGTGCACATCCAGAGCCAGATCAGCCCCATGCCATCATCTTCTCCCCAAC 3606
Db 3490 TACATCCCTGTGCACATCCAGAGCCAGATCAGCCCCATGCCATCATCTTCTCCCCAAC 3549
QY 3607 ACCGAGCGCATGGAGATGCTGTGCTTACGAGGAGGAGGTGTCTAGCTCAACACGTAC 3666
Db 3550 ACCGAGCGCATGGAGATGCTGTGCTTACGAGGAGGAGGTGTCTAGCTCAACACGTAC 3609
QY 3667 GGGCGCATCATTAAGGATGCTGTGCTGAGTGGGGGAGATGCCCTACTTCTGTGSCCTAC 3726
Db 3610 GGGCGCATCATTAAGGATGCTGTGCTGAGTGGGGGAGATGCCCTACTTCTGTGSCCTAC 3669
QY 3727 ATCTGCTCAAACAGATAATGGGCTGGGTGAGAAAGCATTTGAGATCGGCTCTGTGGAG 3786
Db 3670 ATCTGCTCAAACAGATAATGGGCTGGGTGAGAAAGCATTTGAGATCGGCTCTGTGGAG 3729
QY 3787 ACGGGCCACTCGACCGGGCTTTCATGCAACAACAGAGCTCAGAGGCTCAAGTTCCTGTGT 3846
Db 3730 ACGGGCCACTCGACCGGGCTTTCATGCAACAACAGAGCTCAGAGGCTCAAGTTCCTGTGT 3789
QY 3847 GAGCGAAATGACAAAGGTGTTTTTGGCTCAGTCCGCTCTGGGGGACAGCAAGTTTAC 3906
Db 3790 GAGCGAAATGACAAAGGTGTTTTTGGCTCAGTCCGCTCTGGGGGACAGCAAGTTTAC 3849
QY 3907 TTCAATGACTCTGAACCGTAACCTGCATCATGAATGGTGA 3945
Db 3850 TTCAATGACTCTGAACCGTAACCTGCATCATGAATGGTGA 3888

RESULT 2
us-09-688-188b-11

Query Match      95.8%; Score 3785; DB 2; Length 4133;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 3824; Conservative 0; Mismatches 15; Indels 150; Gaps 3;
```



```
QY 2663 ACACAAACCTGCTGACGTGTCAGGCCAGCCACTCACCCACCGAGAAACAGCAAGGCC 2722
Db |||||
QY 2699 ACACAAACCTGCTGACGTGTCAGGCCAGCCACTCACCCACCGAGAAACAGCAAGGCC 2758
Db |||||
QY 2723 AAAGCCCAACCTCGAAAGATGGAGTGGTACTACAGTCTCGTGGGTGGTAAAGGCC 2782
Db |||||
QY 2759 AAAGCCCAACCTCGAAAGATGGAGTGGTACTACAGTCTCGTGGGTGGTAAAGGCC 2818
Db |||||
QY 2783 CTGGCAAGAGTCTGPTCAACGATGTTTGTGATCTAGGGATCTACAGCTCGAGGCAAGTG 2842
Db |||||
QY 2819 CTGGCAAGAGTCTGPTCAACGATGTTTGTGATCTAGGGATCTACAGCTCGAGGCAAGTG 2878
Db |||||
QY 2843 GGGACAGATCCCATCCATCACAGCCCTAGTGGGTGGAGAGGCACTCGGCTCGACCAAGTGC 2902
Db |||||
QY 2879 GGGACAGATCCCATCCATCACAGCCCTAGTGGGTGGAGAGGCACTCGGCTCGACCAAGTGC 2938
Db |||||
QY 2903 AGTACAGTGAAGAGGTCTGTGTGTCACAGTGAATCCACCAACACCGGCCCCACA 2962
Db |||||
QY 2939 AGTACAGTGAAGAGGTCTGTGTGTCACAGTGAATCCACCAACACCGGCCCCACA 2998
Db |||||
QY 2963 GTGACACCCCTGAGATCCGGAAGTACAAAGAGCGATTCAACTCCGAGATCTCTGTGCAG 3022
Db |||||
QY 2999 GTGACACCCCTGAGATCCGGAAGTACAAAGAGCGATTCAACTCCGAGATCTCTGTGCAG 3058
Db |||||
QY 3023 CCTTTGGGGGCTCAACCTGCTGGTGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3082
Db |||||
QY 3059 CCTTTGGGGGCTCAACCTGCTGGTGGCACGGAGAACGGGCTGATGTTGCTGGACCGAA 3118
Db |||||
QY 3083 GTGGCAGGCGAAGGTGTATGGACTCTGTTGGCGCGCAGCTTCACGAGATGATGTGC 3142
Db |||||
QY 3119 GTGGCAGGCGAAGGTGTATGGACTCTGTTGGCGCGCAGCTTCACGAGATGATGTGC 3178
Db |||||
QY 3143 TGGAGGGGCTCAACCTGCTCATCACTCTCAGGGAAAGGAAACAACTGGCGGTGTATT 3202
Db |||||
QY 3179 TGGAGGGGCTCAACCTGCTCATCACTCTCAGGGAAAGGAAACAACTGGCGGTGTATT 3238
Db |||||
QY 3203 ACTGTCTGCTCGGAAACAGATTTGCAATGACCCAGAGTGAGAGAGGAGG 3262
Db |||||
QY 3239 ACTGTCTGCTCGGAAACAGATTTGCAATGACCCAGAGTGAGAGAGGAGG 3298
Db |||||
QY 3263 GTTGACACACCGTGGGGACATGGAGGCTGGGGCACTACCGTGTGTGAAATACAGGC 3322
Db |||||
QY 3299 GTTGACACACCGTGGGGACATGGAGGCTGGGGCACTACCGTGTGTGAAATACAGGC 3358
Db |||||
QY 3323 GAATTAAGTTCCTGTGTCATCGCCCTCAAGAGCTCCGTGGAGGTGATCCCTGGGCCCCCA 3382
Db |||||
QY 3359 GAATTAAGTTCCTGTGTCATCGCCCTCAAGAGCTCCGTGGAGGTGATCCCTGGGCCCCCA 3418
Db |||||
QY 3383 AACCTACCAACAAATTCATGGGCTTCAGTCCCTTTCGGACCTCCGCCACCGCCCTGTC 3442
Db |||||
QY 3419 AACCTACCAACAAATTCATGGGCTTCAGTCCCTTTCGGACCTCCGCCACCGCCCTGTC 3478
Db |||||
QY 3443 TGGTCGACCTGACAGTAGAGGAGGCGCAGCGCTCAAGGTCACTATGGCTCCAGTGTGCTG 3502
Db |||||
QY 3479 TGGTCGACCTGACAGTAGAGGAGGCGCAGCGCTCAAGGTCACTATGGCTCCAGTGTGCTG 3538
Db |||||
QY 3503 GCTTCCATGCTGTGATGTGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3562
Db |||||
QY 3539 GCTTCCATGCTGTGATGTGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACA 3598
Db |||||
QY 3563 TCCAGAGCCAGATCACGCCCTTCCATCATCTTCTCCCAACACCGAGCGCATGGAGA 3622
Db |||||
QY 3599 TCCAGAGCCAGATCACGCCCTTCCATCATCTTCTCCCAACACCGAGCGCATGGAGA 3658
Db |||||
QY 3623 TGTGTGCTGTGCTACGAGGAGCGAGGTGTCTACGTCAACACGTACGGGCGCATCAATTAAG 3682
Db |||||
QY 3659 TGTGTGCTGTGCTACGAGGAGCGAGGTGTCTACGTCAACACGTACGGGCGCATCAATTAAG 3718
Db |||||
QY 3683 ATGTGTGCTGTGCTACGAGGAGCGAGGTGTCTACGTCAACACGTACGGGCGCATCAATTAAG 3742
Db |||||
QY 3719 ATGTGTGCTGTGCTACGAGGAGCGAGGTGTCTACGTCAACACGTACGGGCGCATCAATTAAG 3778
Db |||||
QY 3743 TAATGGGCTGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3802
Db |||||
```

```
Db 3779 TAATGGGCTGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACG 3838
QY 3803 GGGTCTTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3862
Db 3839 GGGTCTTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGG 3898
QY 3863 TGTGTTTTCCTCAGTCCGCTCTGGGGCAGCAGCCAGTTTACTTTCATGACTCTGAACC 3922
Db 3899 TGTGTTTTCCTCAGTCCGCTCTGGGGCAGCAGCCAGTTTACTTTCATGACTCTGAACC 3958
QY 3923 GTAACTGCATCATGAACCTGGTGAAGGGC 3951
Db 3959 GTAACTGCATCATGAACCTGGTGAAGGGC 3987
```

Search completed: August 26, 2004, 15:39:57
Job time : 23 secs

3 Mon Aug 30 09:54:26 2004

us-10-02

```

Db      1201  |||||YIPVHIQSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRIIKDVVLOWGEMPTSVAY 1260
Qy      1241  ICSNQIMGWGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERNDKVFFASVRSGGSSQVY 1300
Db      1261  ICSNQIMGWGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERNDKVFFASVRSGGSSQVY 1320
Qy      1301  FMTLNRNCIMNW 1312
Db      1321  FMTLNRNCIMNW 1332
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 00:54:25 ; Search time 35 Seconds
(without alignments)
1935.236 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

Sequence: 1 MGDPAPARSLDDIDLSALRD.....SGSSQVYFWTLNRNCIMNW 1312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6659	96.1	1326	4	US-09-688-188B-15
2	6659	96.1	1326	4	US-09-291-417D-14
3	4370.5	63.1	1324	4	US-09-645-456A-13
4	4370.5	63.1	1324	4	US-09-425-324A-13
5	4370.5	63.1	1324	4	US-09-645-791-13
6	4360.5	62.9	1332	4	US-09-645-456A-9
7	4360.5	62.9	1332	4	US-09-425-324A-9
8	4360.5	62.9	1332	4	US-09-645-791-9
9	4346	62.7	1353	4	US-09-645-456A-11
10	4346	62.7	1353	4	US-09-425-324A-11
11	4346	62.7	1353	4	US-09-645-791-11
12	4336	62.6	1360	3	US-09-393-569-2
13	4336	62.6	1360	4	US-09-579-664B-14
14	4336	62.6	1360	4	US-09-645-456A-34
15	4336	62.6	1360	4	US-09-425-324A-34
16	4336	62.6	1360	4	US-09-645-791-34
17	4274	61.7	1269	4	US-09-645-456A-15
18	4274	61.7	1269	4	US-09-425-324A-15
19	4274	61.7	1269	4	US-09-645-791-15
20	4264	61.5	1277	4	US-09-645-456A-12
21	4264	61.5	1277	4	US-09-425-324A-12
22	4264	61.5	1277	4	US-09-645-791-12
23	4249.5	61.3	1298	4	US-09-645-456A-14
24	4249.5	61.3	1298	4	US-09-425-324A-14
25	4249.5	61.3	1298	4	US-09-645-791-14
26	4239.5	61.2	1306	4	US-09-645-456A-10
27	4239.5	61.2	1306	4	US-09-425-324A-10

28 4239.5 61.2 1306 4 US-09-645-791-10 Sequence 10, Appl
29 4195.5 60.5 1297 4 US-09-688-188B-14 Sequence 14, Appl
30 4195.5 60.5 1297 4 US-09-291-417D-14 Sequence 14, Appl
31 4021.5 58.0 1239 4 US-09-688-188B-13 Sequence 13, Appl
32 4021.5 58.0 1239 4 US-09-291-417D-13 Sequence 13, Appl
33 3951.5 57.0 1233 4 US-09-688-188B-89 Sequence 89, Appl
34 3951.5 57.0 1233 4 US-09-291-417D-89 Sequence 89, Appl
35 3886.5 56.1 1233 4 US-09-645-456A-35 Sequence 35, Appl
36 3886.5 56.1 1233 4 US-09-425-324A-35 Sequence 35, Appl
37 3886.5 56.1 1233 4 US-09-645-791-35 Sequence 35, Appl
38 2708.5 39.1 1109 4 US-09-688-188B-88 Sequence 88, Appl
39 2708.5 39.1 1109 4 US-09-291-417D-88 Sequence 88, Appl
40 1862.5 26.9 1227 4 US-09-688-188B-105 Sequence 105, App
41 1862.5 26.9 1227 4 US-09-291-417D-105 Sequence 105, App
42 1457 21.0 275 4 US-09-579-664B-8 Sequence 8, Appl
43 1309 18.9 444 3 US-09-221-235-14 Sequence 14, Appl
44 1309 18.9 444 3 US-09-221-928-14 Sequence 14, Appl
45 1309 18.9 444 3 US-09-221-527-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-688-188B-15
; Sequence 15, Application US/09688188B
; Patent No. 6656716

; GENERAL INFORMATION:

; APPLICANT: PLOWMAN, GREGORY

; APPLICANT: MARTINEZ, RICARDO

; APPLICANT: WHITE, DAVID

; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES

; FILE REFERENCE: 038602/0328

; CURRENT APPLICATION NUMBER: US/09/688,188B

; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 09/291,417

; PRIOR FILING DATE: 1999-04-14

; PRIOR APPLICATION NUMBER: 65/081,784

; PRIOR FILING DATE: 1998-04-14

; NUMBER OF SEQ ID NOS: 155

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 1326

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-688-188B-15

Query Match 96.1%; Score 6659; DB 4; Length 1326;

Best Local Similarity 95.8%; Pred. No. 0;

Matches 1270; Conservative 3; Mismatches 3; Indels 50; Gaps 3;

Qy 36 YGQYVGRHVKTGQAAIKVMDVTEDEEIKOEINMLKKYSHRNATYVGAFIKSP 95

Db 2 FGVEYGRHVKTGQAAIKVMDVTEDEEIKOEINMLKKYSHRNATYVGAFIKSP 61

Qy 96 GNDQLWLVNVEFCAGSVTDLVKNTGNALKEDCIAYICREILRGLAHLHAHKVH 155

Db 62 GNDQLWLVNVEFCAGSVTDLVKNTGNALKEDCIAYICREILRGLAHLHAHKVH 121

Qy 156 GQNVLLTENAENVKLVFGVSAQLDRTVGRNTFIGTPYMAPEVIACDENPDATY 215

Db 122 GQNVLLTENAENVKLVFGVSAQLDRTVGRNTFIGTPYMAPEVIACDENPDATY 181

Qy 216 IWSLGTATIMAGAPPLCDMHPMALFLIPNPPRLSKKWKKFIDITCLIKTYL 275

Db 182 IWSLGTATIMAGAPPLCDMHPMALFLIPNPPRLSKKWKKFIDITCLIKTYL 241

Qy 276 SRPPTQLLKFPPIRDQPTQVRIQLKHIDRSRKRGEKEETEYVSGSEEDDSHGE 335

Db 242 SRPPTQLLKFPPIRDQPTQVRIQLKHIDRSRKRGEKEETEYVSGSEEDDSHGE 301

Qy 336 EGFPSSIMNVPGESTIRREFLRLOQKNSALQKQOQOQOQDPEAHIKLLHQRQ 395

Db 336 EGFPSSIMNVPGESTIRREFLRLOQKNSALQKQOQOQOQDPEAHIKLLHQRQ 395

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 00:43:18 ; Search time 154 Seconds
(without alignments)

2407.158 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

Sequence: 1 MGDPAPARSLDDIDLSALRD.....SGSSQVTFMTLRNCINW 1312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	6929	100.0	1312	7 ADE34150	Human mis
2	6660.5	96.1	1295	5 AAO18508	Human ins
3	6659	96.1	1326	2 AAY55933	Human ZC3
4	6646.5	95.9	1303	4 AAM79153	Human pro
5	6646.5	95.9	1303	5 AAO18507	Human ins
6	6628.5	95.7	1303	4 AAE10612	Human nov
7	6622	95.6	1332	4 AAE10611	Human nov
8	6603.5	95.3	1276	7 ADE34154	Human mis
9	6311	91.1	1244	4 AAE10614	Human nov
10	6304.5	91.0	1273	4 AAE10613	Human nov
11	5651	81.6	1701	4 ABG24020	Novel hum
12	4370.5	63.1	1324	4 AAB68221	Amino aci
13	4360.5	62.9	1332	4 AAB68217	Amino aci
14	4346	62.7	1353	4 AAB68219	Amino aci
15	4336	62.6	1360	3 AAB85283	Amino aci
16	4336	62.6	1360	4 AAB50059	Large NIK
17	4336	62.6	1360	5 AAO18506	Human ins
18	4336	62.6	1385	7 ADD14162	Human src
19	4325	62.4	1385	4 AAM79405	Human pro
20	4274	61.7	1268	7 ADE31765	Human 154
21	4274	61.7	1269	4 AAB68223	Amino aci
22	4264	61.5	1277	4 AAB68220	Amino aci
23	4249.5	61.3	1298	4 AAB68222	Amino aci
24	4244	61.2	1339	4 AAM78421	Human pro
25	4239.5	61.2	1306	4 AAB68218	Amino aci

26	4195.5	60.5	1297	2 AAY55932	Human ZC2
27	4021.5	58.0	1239	2 AAY55931	Human ZC1
28	3977	57.4	1212	4 AAE04368	Human kin
29	3977	57.4	1212	7 ADE35753	Human pro
30	3960.5	57.2	1165	3 AAB34016	Human ORF
31	3951.5	57.0	1233	2 AAY55954	Mouse STE
32	3872.5	55.9	1165	4 ABG17470	Novel hum
33	3872.5	55.9	1165	5 AAO18509	Human ins
34	3872.5	55.9	1165	6 ABU03499	Angiogene
35	3824	55.2	1175	4 ABG17468	Novel hum
36	3824	55.2	1175	5 AAU76512	Human, HPK
37	3821	55.1	792	7 ADE34152	Human mis
38	3807.5	55.0	1655	4 ABG17466	Novel hum
39	3777.5	54.5	1135	3 AAY68784	Amino aci
40	3694.5	53.3	1219	4 ABG17469	Novel hum
41	2708.5	39.1	1109	2 AAY55953	Nematode
42	2280	32.9	510	3 AAB54144	Human, pan
43	1862.5	26.9	1227	2 AAY55965	Full leng
44	1819.5	26.3	1581	5 AAE24145	Human kin
45	1686	24.3	425	4 AAB92792	Human pro

ALIGNMENTS

RESULT 1
ADE34150
ID ADE34150 standard; protein; 1312 AA.
XX ADE34150;
XX
XX
DT 29-JAN-2004 (first entry)
XX
DE Human mishapen/NIKS-related kinase, Mink3a.
XX
KW Human; mishapen/NIKS-related kinase; Mink3a; enzyme; antiinflammatory;
KW immunosuppressive; cytostatic; germinal centre kinase;
KW c-JUN N-terminal kinase; JNK; extracellular signal response kinase; ERK;
KW growth factor induced-ERK activation; proliferation;
KW cell proliferation disorder; cell survival;
KW intracellular signal transduction; apoptosis; morphological change;
KW cell migration; gene therapy; inflammatory disease; autoimmune disease;
KW immunodeficiency; cancer.
XX
XX Homo sapiens.
XX
XX US2003077597-A1.
XX
PD 24-APR-2003.
XX
XX 19-OCT-2001; 2001US-00029115.
XX
XX 19-OCT-2001; 2001US-00029115.
XX
XX (LUOY/) LUO Y.
XX (FUCA/) FU C A.
XX (SHEN/) SHEN M.
XX
XX Luo Y, Fu CA, Shen M;
XX
XX WPI; 2003-635076/60.
XX N-PSDB; ADE34151.
XX
XX New mishapen/NIKS-related kinase nucleic acids and proteins useful in
XX gene therapy and for treating disorders, e.g. acute and chronic
XX inflammatory diseases.
XX
XX Claim 5; SEQ ID NO 2; 53pp; English.
XX
XX The invention relates to a recombinant nucleic acid capable of
XX hybridising to a Human DNA encoding mishapen/NIKS-related kinase
XX (Mink3a, 3b and 3c, germinal centre kinase proteins) appearing as
XX ADE34151, ADE34153 and ADE34155, or at least 90% identity to them, or

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 00:43:54 ; Search time 29 Seconds
(without alignments)
2355.726 Million cell updates/sec

Title: US-10-029-115-2
Perfect score: 6929
Sequence: 1 MGDPAPARSLDLDLSALRD.....SGSSQVFMNLNRCINMW 1312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	6909	99.7	1332	1 M4K6 HUMAN	Q8N4C8 homo sapien
2	6464	93.3	1308	1 M4K6 MOUSE	Q9JMS2 mus musculus
3	4336	62.6	1360	1 TN1K HUMAN	Q9U8E5 homo sapien
4	4017.5	58.0	1239	1 M4K4 HUMAN	O95819 homo sapien
5	3951.5	57.0	1233	1 M4K4 MOUSE	P97820 mus musculus
6	3286	47.4	916	1 TN1K MOUSE	P83510 mus musculus
7	2646	38.2	1080	1 M115 CAEL	Q23356 caenorhabdi
8	738	10.7	894	1 M4K3 HUMAN	Q81VH8 homo sapien
9	729	10.5	862	1 M4K3 RAT	Q924I2 rattus norv
10	715.5	10.3	487	1 STK3 HUMAN	Q13043 homo sapien
11	694.5	10.0	491	1 STK3 HUMAN	Q13188 homo sapien
12	693.5	10.0	669	1 HPO DROME	Q8T0S6 drosophila
13	691	10.0	847	1 M4K5 MOUSE	Q8BPM2 mus musculus
14	687	9.9	846	1 M4K5 HUMAN	O9Y4K4 homo sapien
15	681.5	9.8	426	1 ST25 HUMAN	O00506 homo sapien
16	675.5	9.7	426	1 ST25 MOUSE	Q922W1 mus musculus
17	667	9.6	1080	1 NRK1 YEAST	P38692 saccharomyc
18	660.5	9.5	833	1 M4K1 HUMAN	Q92918 homo sapien
19	656.5	9.5	443	1 ST24 HUMAN	O9Y6E0 homo sapien
20	653.5	9.4	819	1 M4K2 HUMAN	Q12851 h mitogen-a
21	644	9.3	968	1 STKA HUMAN	O94804 homo sapien
22	638	9.2	821	1 M4K2 MOUSE	Q61161 mus musculus
23	636.5	9.2	966	1 STKA MOUSE	O55098 mus musculus
24	630.5	9.1	881	1 M4K3 MOUSE	Q99JP0 mus musculus
25	629	9.1	827	1 M4K1 MOUSE	P70218 mus musculus
26	620.5	9.0	1501	1 NINC DROME	P10676 drosophila
27	552	8.0	471	1 SIDA SCHPO	O14305 schizosacch
28	551	8.0	982	1 SULU CAEL	P46549 caenorhabdi
29	548	7.9	490	1 SP51 YEAST	P08458 saccharomyc
30	532.5	7.7	658	1 PAK1 YEAST	F50527 schizosacch
31	507	7.3	971	1 CLA4 CANAL	O14427 candida alb
32	505	7.3	652	1 NAK1 SCHPO	O75011 schizosacch
33	504	7.3	556	1 SPAK_MOUSE	Q921W9 mus musculus

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database : SwissProt_42.*

Result No. Query Match Length ID Description

1 6909 99.7 1332 1 M4K6 HUMAN Q8N4C8 homo sapien

2 6464 93.3 1308 1 M4K6 MOUSE Q9JMS2 mus musculus

3 4336 62.6 1360 1 TN1K HUMAN Q9U8E5 homo sapien

4 4017.5 58.0 1239 1 M4K4 HUMAN O95819 homo sapien

5 3951.5 57.0 1233 1 M4K4 MOUSE P97820 mus musculus

6 3286 47.4 916 1 TN1K MOUSE P83510 mus musculus

7 2646 38.2 1080 1 M115 CAEL Q23356 caenorhabdi

8 738 10.7 894 1 M4K3 HUMAN Q81VH8 homo sapien

9 729 10.5 862 1 M4K3 RAT Q924I2 rattus norv

10 715.5 10.3 487 1 STK3 HUMAN Q13043 homo sapien

11 694.5 10.0 491 1 STK3 HUMAN Q13188 homo sapien

12 693.5 10.0 669 1 HPO DROME Q8T0S6 drosophila

13 691 10.0 847 1 M4K5 MOUSE Q8BPM2 mus musculus

14 687 9.9 846 1 M4K5 HUMAN O9Y4K4 homo sapien

15 681.5 9.8 426 1 ST25 HUMAN O00506 homo sapien

16 675.5 9.7 426 1 ST25 MOUSE Q922W1 mus musculus

17 667 9.6 1080 1 NRK1 YEAST P38692 saccharomyc

18 660.5 9.5 833 1 M4K1 HUMAN Q92918 homo sapien

19 656.5 9.5 443 1 ST24 HUMAN O9Y6E0 homo sapien

20 653.5 9.4 819 1 M4K2 HUMAN Q12851 h mitogen-a

21 644 9.3 968 1 STKA HUMAN O94804 homo sapien

22 638 9.2 821 1 M4K2 MOUSE Q61161 mus musculus

23 636.5 9.2 966 1 STKA MOUSE O55098 mus musculus

24 630.5 9.1 881 1 M4K3 MOUSE Q99JP0 mus musculus

25 629 9.1 827 1 M4K1 MOUSE P70218 mus musculus

26 620.5 9.0 1501 1 NINC DROME P10676 drosophila

27 552 8.0 471 1 SIDA SCHPO O14305 schizosacch

28 551 8.0 982 1 SULU CAEL P46549 caenorhabdi

29 548 7.9 490 1 SP51 YEAST P08458 saccharomyc

30 532.5 7.7 658 1 PAK1 YEAST F50527 schizosacch

31 507 7.3 971 1 CLA4 CANAL O14427 candida alb

32 505 7.3 652 1 NAK1 SCHPO O75011 schizosacch

33 504 7.3 556 1 SPAK_MOUSE Q921W9 mus musculus

ALIGNMENTS

RESULT 1

M4K6 HUMAN

ID	M4K6 HUMAN	STANDARD;	PRT;	1332 AA.
AC	Q8N4C8; Q9PLX1; Q9P2R8;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Mitogen-activated protein kinase kinase kinase 6 (EC 2.7.1.37)			
DE	(MAPK/ERK kinase kinase kinase 6) (MEK kinase kinase 6) (MEKKK 6)			
DE	(Misshapen/NIK-related kinase) (CCK family kinase MINK).			
GN	M4K6 OR MINK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_taxID=9606;			
RN	[1]_taxID=9606;			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Brain;			
RX	MEDLINE=20175403; PubMed=10708748;			
RA	Dan I., Watanabe N.M., Kobayashi T., Yamashita-Suzuki K., Fukagaya Y.,			
RA	Kajikawa E., Kimura W.K., Nakashima T.M., Matsumoto K.,			
RA	Ninomiya-Tsujii J., Kusumi A.;			
RT	"Molecular cloning of MINK, a novel member of mammalian GCK family			
RT	kinases, which is up-regulated during postnatal mouse cerebral			
RT	development."			
RL	FEBS Lett. 469:19-23 (2000).			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RC	TISSUE=Lymph;			
RC	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Heltan E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.N., Krzywinski M.I., Skalska U., Smalish D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
CC	!- FUNCTION: Serine/threonine kinase that may play a role in the			
CC	response to environmental stress. Appears to act upstream of the			
CC	c-jun N-terminal pathway (By similarity).			
CC	!- FUNCTION: May play a role in the development of the brain (By			
CC	similarity).			
CC	!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a			

34	502	7.2	553	1	SPAK_RAT	O88506 rattus norv
35	500.5	7.2	547	1	SPAK_HUMAN	Q9uew8 homo sapien
36	498.5	7.2	544	1	PAK3_HUMAN	O75914 homo sapien
37	498.5	7.2	544	1	PAK3_RAT	O62829 rattus norv
38	496	7.2	544	1	PAK1_RAT	P35485 rattus norv
39	496	7.2	545	1	PAK1_HUMAN	Q13153 homo sapien
40	495.5	7.2	842	1	CLA4_YEAST	P48562 saccharomyc
41	494	7.1	545	1	PAK1_MOUSE	O88643 mus musculus
42	493.5	7.1	544	1	PAK3_MOUSE	O61036 mus musculus
43	488	7.0	589	1	SHK2_SCHPO	Q10056 schizosacch
44	482	7.0	524	1	PAK2_HUMAN	Q13177 homo sapien
45	481.5	6.9	524	1	PAK2_RAT	Q64303 rattus norv

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 00:50:59 ; Search time 157 Seconds
(without alignments)
2636.687 Million cell updates/sec

Title: US-10-029-115-2
Perfect score: 6929
Sequence: 1 MGDPAPARSLDDLDLALRD.....SGSSQVYFWTLNRCNMW 1312

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTRMBL_25:*
- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6701	96.7	1334	11	Q7TT13
2	4189.5	60.5	1303	13	Q7SY42
3	2805.5	40.5	1550	5	Q9W002
4	2698	38.9	1082	5	Q8T8M3
5	2696.5	38.9	1087	5	Q9XYC3
6	2692	38.9	1096	5	Q95217
7	2661	38.4	1072	5	Q814B5
8	1855	26.8	1582	4	Q7Z4L4
9	1826	26.4	1582	4	Q7Z2Y5
10	1702.5	24.6	1455	11	Q9R0G8
11	1701.5	24.6	1455	11	Q9R0S4
12	1551	22.4	292	4	Q9H8M9
13	1458	21.0	792	5	Q9UAN7
14	1377	19.9	728	5	Q9XYC4
15	993	14.3	334	11	Q8C9S9
16	829.5	12.0	169	11	Q61155

17	811.5	11.7	1219	5	Q9V8R6
18	804.5	11.6	1615	4	Q9NVS8
19	804.5	11.6	1616	4	Q8NEV4
20	800.5	11.6	1613	11	Q8K3H5
21	795	11.5	1775	13	Q9DXG6
22	779	11.2	1838	13	Q9DG88
23	765	11.0	1310	13	Q800Q6
24	764.5	11.0	1192	4	Q8IX64
25	764.5	11.0	1251	4	Q8IX68
26	764.5	11.0	1275	4	Q8IX65
27	764.5	11.0	1278	4	Q8WXR4
28	764.5	11.0	1314	4	Q8IX66
29	764.5	11.0	1341	4	Q8IX67
30	761.5	11.0	1113	4	Q96N94
31	734	10.6	737	5	Q86IX1
32	734	10.6	829	3	Q87IH9
33	720	10.4	825	10	Q8SAE1
34	718	10.4	825	10	Q9ARL7
35	713.5	10.3	487	11	Q9J111
36	712	10.3	950	13	Q9YHC9
37	711.5	10.3	842	10	Q9FNU3
38	710	10.2	836	10	Q24527
39	707.5	10.2	1120	10	Q9LQAL
40	703	10.1	491	13	Q802A6
41	701.5	10.1	497	11	Q9J110
42	701.5	10.1	539	11	Q80UG4
43	701	10.1	947	5	Q8SVL1
44	700	10.1	651	5	Q9SZN6
45	700	10.1	947	5	Q8MLI8

ALIGNMENTS

RESULT 1

ID	Q7TT13	PRELIMINARY;	PRT;	1334	AA.
AC	Q7TT13;				
DC	01-OCT-2003 (TrEMBLrel. 25, Created)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6; TISSUE=Brain;				
RX	MEDLINE=22388257; Pubmed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Varusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6; TISSUE=Brain;				

Q9V8R6	drosophila
Q9NVS8	homo sapien
Q8NEV4	homo sapien
Q8K3H5	mus musculus
Q9DXG6	brachydanio
Q9DG88	morone saxa
Q800Q6	morone saxa
Q8IX64	homo sapien
Q8IX68	homo sapien
Q8IX65	homo sapien
Q8WXR4	homo sapien
Q8IX66	homo sapien
Q8IX67	homo sapien
Q96N94	homo sapien
Q86IX1	dictyosteli
Q87IH9	neurospora
Q8SAE1	triticum mo
Q9ARL7	hordeum vul
Q9J111	mus musculus
Q9YHC9	xenopus lae
Q9FNU3	oryza sativ
Q24527	arabidopsis
Q9LQAL	arabidopsis
Q802A6	squalus aca
Q9J110	mus musculus
Q80UG4	mus musculus
Q8SVL1	drosophila
Q9SZN6	caenorhabdi
Q8MLI8	drosophila

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 00:52:04 ; Search time 53 seconds
(without alignments)
2381.194 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

Sequence: 1 MGDPAFARSLDDLSALRD.....SGSGQVYFMTLNRNCIMNW 1312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3951.5	57.0	1233	2 T30989	serine/threonine p
2	3008.5	43.4	1102	2 JG6316	probable protein k
3	2647.5	38.2	1075	2 T27622	hypothetical prote
4	2646	38.2	1080	2 T27622	hypothetical prote
5	2403.5	34.7	1027	2 T46481	hypothetical prote
6	1458	21.0	792	2 T43630	serine/threonine p
7	1377	19.9	728	2 T43632	serine/threonine p
8	710	10.2	836	2 B96716	probable serine/th
9	698	10.1	653	2 T34356	hypothetical prote
10	688.5	9.9	1233	2 T1457	serine/threonine p
11	678.5	9.8	426	2 S71886	Ste20-like protein
12	670	9.7	1231	2 T18532	serine/threonine pr
13	667	9.6	1080	2 S48944	hypothetical prote
14	658	9.5	1001	2 T17365	serine/threonine p
15	653.5	9.4	819	2 A53714	protein kinase (5C
16	651.5	9.4	1206	2 T34021	protein kinase SK2
17	640.5	9.2	829	2 T29372	hypothetical prote
18	635.5	9.2	690	2 C96572	protein F12M16.4 (
19	616.5	8.9	1135	1 A29813	132k ninaC protein
20	616.5	8.9	1501	1 T28913	174k ninaC protein
21	588.5	8.5	1228	2 T18897	hypothetical prote
22	592.5	8.4	1014	2 T31109	myosin III - Atlan
23	552	8.0	471	2 T39232	probable serine th
24	551	8.0	982	2 T18576	serine-threonine k
25	548	7.9	490	2 S47946	protein kinase hom
26	535	7.7	312	2 T38525	serine/threonine p
27	533.5	7.7	658	2 T39500	serine/threonine-s
28	505	7.3	652	2 T39722	serine/threonine p
29	504.5	7.3	658	2 S60170	protein kinase fak

30	501.5	7.2	561	2 T51417	protein kinase-lik
31	498.5	7.2	544	2 A57597	beta-p21-activated
32	497	7.2	710	2 T13458	hypothetical prote
33	496	7.2	544	2 S40482	serine/threonine-s
34	496	7.2	545	2 G01773	p21-activated prot
35	495.5	7.2	842	2 S60402	protein kinase CLA
36	493.5	7.1	544	2 T49376	p21 activated kina
37	489	7.1	553	2 T01479	hypothetical prote
38	488	7.0	589	2 T38066	serine/threonine-p
39	481.5	6.9	525	2 S58682	protein kinase, p2
40	478.5	6.9	622	2 T15467	hypothetical prote
41	478.5	6.9	655	2 S51884	probable protein k
42	474.5	6.8	378	2 T26684	hypothetical prote
43	463	6.7	693	2 B85112	hypothetical prote
44	459	6.6	939	2 S28394	probable serine/th
45	455	6.6	607	2 T01904	hypothetical prote

ALIGNMENTS

RESULT 1

T30989
serine/threonine protein kinase NIK - mouse
N:Alternate names: NCK interacting kinase
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30989
R:Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.
EMBO J. 16, 1279-1290, 1997
A:Title: NIK is a new Ste20-related kinase that binds NCK and MEK1 and activates the
A:Reference number: 220954; MUID:97280817; PMID:9135144
A:Accession: T30989
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1233 <SU>
A:Cross-references: EMBL:U88984; NID:g1872545; PID:g1872546; PIDN:AAC53165.1
C:Keywords: protein kinase

Query Match 57.0%; Score 3951.5; DB 2; Length 1233;
Best Local Similarity 62.3%; Pred. No. 1.8e-105;
Matches 846; Conservative 112; Mismatches 228; Indels 173; Gaps 32;

Qy	1	MGDPAPARSLDDLSALRDPA	GIFELVEVVGNGTYGVYKGRHVTGQ	LAALKVMDVTE	60
Db	1	MANDSPAKSLVDLDSLRDP	AGIFELVEVVGNGTYGVYKGRHVT	-VTAAIKVMDVTE	59
Qy	61	DEEEIKQEIINMLKKYSHRN	IATYTGAFIKKPPGNDQDLVW	MFPCGAGSVTDLVKNT	120
Db	60	DEEEITLEINMLKKYSHRN	IATYTGAFIKKPPGDDQDLVW	MFPCGAGSITDLVNT	119
Qy	121	KGNALDEDCIATYCRILRGL	AHLHAKVTHRDIKQNVLLTEN	AEVKLVDFGVSAQLDR	180
Db	120	KGNTLKEDWIATYSREILRGL	AHLHIVHVDIKQNVLLTEN	AEVKLVDFGVSAQLDR	179
Qy	181	TVGRRNTFTGTPVWMAPEV	IACDENPDATYVRSYDTSW	LSGITAIENAEAGPLCDMHP	240
Db	180	TVGRRNTFTGTPVWMAPEV	IACDENPDATYVRSYDTSW	LSGITAIENAEAGPLCDMHP	239
Qy	241	ALFLIPRNPPLKSKKSKK	FFIDFTDTCIKTYLSRPPTE	QQLKPFPRDQPTERQVRI	300
Db	240	ALFLIPRNPPLKSKKSKK	FFIEGCLVKNYMQRPSTEQ	LLKHPFRDQPNREQVRI	299
Qy	301	QLQKHIDRKKKGEKEETE	YYSGSEEDDSDHGE-EGEP	SSIMNVPGESTURRFLRLQ	359
Db	300	QLQKHIDRKKKGEKDETE	YYSGSEEEVPEQGEPS	SVNVPGESTLRLDFLRLQ	359
Qy	360	QENKNSSEALKQQQQQQQ	QDPEAHIKHLHQRIIEE	QEKERRRVEEQRRERQR	419
Db	360	QENKNSSEALRQQLQEQ	QLAEQYKQLAEKQIEQ	QKQRRRLERQRRERAR	419
Qy	420	KLOEKQ-----QRLE	DMQALR-----EERR	QAEQYKQKL-EQQRSE	463

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2004, 00:57:10 ; Search time 81 seconds
(without alignments)
5095.952 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 6929

Sequence: 1 MGDPAFARSLDDIDLSALRD.....SGSSQVYFMTLNRCINMW 1312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6929	100.0	1312	14	US-10-029-115-2
2	6660.5	96.1	1295	10	US-09-789-390-30
3	6660.5	96.1	1295	10	US-09-789-390-32
4	6660.5	96.1	1295	10	US-09-789-390-34
5	6660.5	96.1	1295	10	US-09-789-390-37
6	6660.5	96.1	1295	10	US-09-789-390-39
7	6659	96.1	1326	10	US-09-291-417-15
8	6646.5	95.9	1303	10	US-09-789-390-35
9	6646.5	95.9	1303	10	US-09-789-390-38
10	6628.5	95.7	1303	10	US-09-789-390-7
11	6622	95.6	1332	10	US-09-789-390-9
12	6603.5	95.3	1276	14	US-10-029-115-6
13	6311	91.1	1244	10	US-09-789-390-13
14	6304.5	91.0	1273	10	US-09-789-390-11
15	5422.5	78.3	1303	10	US-09-789-390-65

ALIGNMENTS

RESULT 1

US-10-029-115-2
; Sequence 2, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-115-2

Query Match	100.0%;	Score 6929;	DB 14;	Length 1312;
Best Local Similarity	100.0%;	Pred. No. 4.4e-311;		
Matches 1312;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGDPAPARSLDDIDLALRDPAGIFELVEVVGNGTYGVYKGRHVKTGQLAAIKVMDVTE	60	
Db	1	MGDPAPARSLDDIDLALRDPAGIFELVEVVGNGTYGVYKGRHVKTGQLAAIKVMDVTE	60	
QY	61	DEEETIKQEINMLKYSKSHRNATYTGAFIKKSPGNDQDLWLVNMFPGAGSVTDLVKNT	120	
Db	61	DEEETIKQEINMLKYSKSHRNATYTGAFIKKSPGNDQDLWLVNMFPGAGSVTDLVKNT	120	
QY	121	KGNAKEDCITAYICREILGLAHLHAHKVIHREDIKQGVLLTENAELVKLVDFGVSAQLDR	180	
Db	121	KGNAKEDCITAYICREILGLAHLHAHKVIHREDIKQGVLLTENAELVKLVDFGVSAQLDR	180	
QY	181	TVGRNRTFTGPTWMAPEVIACDNPDATYDYSRDSVLSLGTATBMAEGAPPLCDMPMR	240	

Sequence 63, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 67, Appl
Sequence 68, Appl
Sequence 2, Appl
Sequence 14, Appl
Sequence 122, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 9, Appl
Sequence 157, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 126, Appl
Sequence 224, Appl
Sequence 225, Appl
Sequence 226, Appl
Sequence 4, Appl
Sequence 88, Appl
Sequence 1181, Appl
Sequence 596, Appl
Sequence 105, Appl
Sequence 134, Appl
Sequence 133, Appl
Sequence 135, Appl
Sequence 79, Appl
Sequence 1920, Appl
Sequence 8, Appl